

05092
#2
OIPE
1-4-01RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/692,504DATE: 11/02/2000
TIME: 13:57:01Input Set : A:\P1748R1.txt
Output Set: N:\CRF3\11022000\I692504.raw

ENTERED

3 <110> APPLICANT: De Sauvage, Frederic
 4 Grewal, Iqbal
 5 Gurney, Austin L.
 7 <120> TITLE OF INVENTION: TYPE I CYTOKINE RECEPTOR TCCR
 9 <130> FILE REFERENCE: P1748R1
 W--> 11 <140> CURRENT APPLICATION NUMBER: US/09/692,504
 11 <141> CURRENT FILING DATE: 2000-10-18
 13 <150> PRIOR APPLICATION NUMBER: US 60/160,542
 14 <151> PRIOR FILING DATE: 1999-10-20
 16 <160> NUMBER OF SEQ ID NOS: 16
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 636
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Homo sapiens
 23 <400> SEQUENCE: 1
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 25 1 5 10 15
 27 Lys Leu Ala Leu Leu Pro Leu Leu Trp Val Leu Phe Gln Arg Thr
 28 20 25 30
 30 Arg Pro Gln Gly Ser Ala Gly Pro Leu Gln Cys Tyr Gly Val Gly
 31 35 40 45
 33 Pro Leu Gly Asp Leu Asn Cys Ser Trp Glu Pro Leu Gly Asp Leu
 34 50 55 60
 36 Gly Ala Pro Ser Glu Leu His Leu Gln Ser Gln Lys Tyr Arg Ser
 37 65 70 75
 39 Asn Lys Thr Gln Thr Val Ala Val Ala Ala Gly Arg Ser Trp Val
 40 80 85 90
 42 Ala Ile Pro Arg Glu Gln Leu Thr Met Ser Asp Lys Leu Leu Val
 43 95 100 105
 45 Trp Gly Thr Lys Ala Gly Gln Pro Leu Trp Pro Pro Val Phe Val
 46 110 115 120
 48 Asn Leu Glu Thr Gln Met Lys Pro Asn Ala Pro Arg Leu Gly Pro
 49 125 130 135
 51 Asp Val Asp Phe Ser Glu Asp Asp Pro Leu Glu Ala Thr Val His
 52 140 145 150
 54 Trp Ala Pro Pro Thr Trp Pro Ser His Lys Val Leu Ile Cys Gln
 55 155 160 165
 57 Phe His Tyr Arg Arg Cys Gln Glu Ala Ala Trp Thr Leu Leu Glu
 58 170 175 180
 60 Pro Glu Leu Lys Thr Ile Pro Leu Thr Pro Val Glu Ile Gln Asp
 61 185 190 195
 63 Leu Glu Leu Ala Thr Gly Tyr Lys Val Tyr Gly Arg Cys Arg Met
 64 200 205 210
 66 Glu Lys Glu Glu Asp Leu Trp Gly Glu Trp Ser Pro Ile Leu Ser
 67 215 220 225
 69 Phe Gln Thr Pro Pro Ser Ala Pro Lys Asp Val Trp Val Ser Gly
 70 230 235 240

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72 Asn Leu Cys Gly Thr Pro Gly Gly Glu Glu Pro Leu Leu Leu Trp
73                               245          250          255
75 Lys Ala Pro Gly Pro Cys Val Gln Val Ser Tyr Lys Val Trp Phe
76                               260          265          270
78 Trp Val Gly Gly Arg Glu Leu Ser Pro Glu Gly Ile Thr Cys Cys
79                               275          280          285
81 Cys Ser Leu Ile Pro Ser Gly Ala Glu Trp Ala Arg Val Ser Ala
82                               290          295          300
84 Val Asn Ala Thr Ser Trp Glu Pro Leu Thr Asn Leu Ser Leu Val
85                               305          310          315
87 Cys Leu Asp Ser Ala Ser Ala Pro Arg Ser Val Ala Val Ser Ser
88                               320          325          330
90 Ile Ala Gly Ser Thr Glu Leu Leu Val Thr Trp Gln Pro Gly Pro
91                               335          340          345
93 Gly Glu Pro Leu Glu His Val Val Asp Trp Ala Arg Asp Gly Asp
94                               350          355          360
96 Pro Leu Glu Lys Leu Asn Trp Val Arg Leu Pro Pro Gly Asn Leu
97                               365          370          375
99 Ser Ala Leu Leu Pro Gly Asn Phe Thr Val Gly Val Pro Tyr Arg
100                              380          385          390
102 Ile Thr Val Thr Ala Val Ser Ala Ser Gly Leu Ala Ser Ala Ser
103                              395          400          405
105 Ser Val Trp Gly Phe Arg Glu Glu Leu Ala Pro Leu Val Gly Pro
106                              410          415          420
108 Thr Leu Trp Arg Leu Gln Asp Ala Pro Pro Gly Thr Pro Ala Ile
109                              425          430          435
111 Ala Trp Gly Glu Val Pro Arg His Gln Leu Arg Gly His Leu Thr
112                              440          445          450
114 His Tyr Thr Leu Cys Ala Gln Ser Gly Thr Ser Pro Ser Val Cys
115                              455          460          465
117 Met Asn Val Ser Gly Asn Thr Gln Ser Val Thr Leu Pro Asp Leu
118                              470          475          480
120 Pro Trp Gly Pro Cys Glu Leu Trp Val Thr Ala Ser Thr Ile Ala
121                              485          490          495
123 Gly Gln Gly Pro Pro Gly Pro Ile Leu Arg Leu His Leu Pro Asp
124                              500          505          510
126 Asn Thr Leu Arg Trp Lys Val Leu Pro Gly Ile Leu Phe Leu Trp
127                              515          520          525
129 Gly Leu Phe Leu Leu Gly Cys Gly Leu Ser Leu Ala Thr Ser Gly
130                              530          535          540
132 Arg Cys Tyr His Leu Arg His Lys Val Leu Pro Arg Trp Val Trp
133                              545          550          555
135 Glu Lys Val Pro Asp Pro Ala Asn Ser Ser Ser Gly Gln Pro His
136                              560          565          570
138 Met Glu Gln Val Pro Glu Ala Gln Pro Leu Gly Asp Leu Pro Ile
139                              575          580          585
141 Leu Glu Val Glu Glu Met Glu Pro Pro Pro Val Met Glu Ser Ser
142                              590          595          600
144 Gln Pro Ala Gln Ala Thr Ala Pro Leu Asp Ser Gly Tyr Glu Lys

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```

145           605           610           615
147 His Phe Leu Pro Thr Pro Glu Glu Leu Gly Leu Leu Gly Pro Pro
148           620           625           630
150 Arg Pro Gln Val Leu Ala
151           635
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 623
155 <212> TYPE: PRT
156 <213> ORGANISM: Mus musculus
158 <400> SEQUENCE: 2
159 Met Asn Arg Leu Arg Val Ala Arg Leu Thr Pro Leu Glu Leu Leu
160 1 5 10 15
162 Leu Ser Leu Met Ser Leu Leu Leu Gly Thr Arg Pro His Gly Ser
163 20 25 30
165 Pro Gly Pro Leu Gln Cys Tyr Ser Val Gly Pro Leu Gly Ile Leu
166 35 40 45
168 Asn Cys Ser Trp Glu Pro Leu Gly Asp Leu Glu Thr Pro Pro Val
169 50 55 60
171 Leu Tyr His Gln Ser Gln Lys Tyr His Pro Asn Arg Val Trp Glu
172 65 70 75
174 Val Lys Val Pro Ser Lys Gln Ser Trp Val Thr Ile Pro Arg Glu
175 80 85 90
177 Gln Phe Thr Met Ala Asp Lys Leu Leu Ile Trp Gly Thr Gln Lys
178 95 100 105
180 Gly Arg Pro Leu Trp Ser Ser Val Ser Val Asn Leu Glu Thr Gln
181 110 115 120
183 Met Lys Pro Asp Thr Pro Gln Ile Phe Ser Gln Val Asp Ile Ser
184 125 130 135
186 Glu Glu Ala Thr Leu Glu Ala Thr Val Gln Trp Ala Pro Pro Val
187 140 145 150
189 Trp Pro Pro Gln Lys Ala Leu Thr Cys Gln Phe Arg Tyr Lys Glu
190 155 160 165
192 Cys Gln Ala Glu Ala Trp Thr Arg Leu Glu Pro Gln Leu Lys Thr
193 170 175 180
195 Asp Gly Leu Thr Pro Val Glu Met Gln Asn Leu Glu Pro Gly Thr
196 185 190 195
198 Cys Tyr Gln Val Ser Gly Arg Cys Gln Val Glu Asn Gly Tyr Pro
199 200 205 210
201 Trp Gly Glu Trp Ser Ser Pro Leu Ser Phe Gln Thr Pro Phe Leu
202 215 220 225
204 Asp Pro Glu Asp Val Trp Val Ser Gly Thr Val Cys Glu Thr Ser
205 230 235 240
207 Gly Lys Arg Ala Ala Leu Leu Val Trp Lys Asp Pro Arg Pro Cys
208 245 250 255
210 Val Gln Val Thr Tyr Thr Val Trp Phe Gly Ala Gly Asp Ile Thr
211 260 265 270
213 Thr Thr Gln Glu Glu Val Pro Cys Cys Lys Ser Pro Val Pro Ala
214 275 280 285
216 Trp Met Glu Trp Ala Val Val Ser Pro Gly Asn Ser Thr Ser Trp

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217		290		295		300
219	Val Pro Pro Thr	Asn Leu Ser Leu Val	Cys Leu Ala Pro Glu Ser			
220		305		310		315
222	Ala Pro Cys Asp	Val Gly Val Ser Ser	Ala Asp Gly Ser Pro Gly			
223		320		325		330
225	Ile Lys Val Thr	Trp Lys Gln Gly Thr	Arg Lys Pro Leu Glu Tyr			
226		335		340		345
228	Val Val Asp Trp	Ala Gln Asp Gly Asp	Ser Leu Asp Lys Leu Asn			
229		350		355		360
231	Trp Thr Arg Leu	Pro Pro Gly Asn Leu Ser	Thr Leu Leu Pro Gly			
232		365		370		375
234	Glu Phe Lys Gly	Gly Val Pro Tyr Arg	Ile Thr Val Thr Ala Val			
235		380		385		390
237	Tyr Ser Gly Gly	Leu Ala Ala Ala Pro	Ser Val Trp Gly Phe Arg			
238		395		400		405
240	Glu Glu Leu Val	Pro Leu Ala Gly Pro	Ala Val Trp Arg Leu Pro			
241		410		415		420
243	Asp Asp Pro Pro	Gly Thr Pro Val Val	Ala Trp Gly Glu Val Pro			
244		425		430		435
246	Arg His Gln Leu	Arg Gly Gln Ala Thr	His Tyr Thr Phe Cys Ile			
247		440		445		450
249	Gln Ser Arg Gly	Leu Ser Thr Val Cys	Arg Asn Val Ser Ser Gln			
250		455		460		465
252	Thr Gln Thr Ala	Thr Leu Pro Asn Leu	His Ser Gly Ser Phe Lys			
253		470		475		480
255	Leu Trp Val Thr	Val Ser Thr Val Ala	Gly Gln Gly Pro Pro Gly			
256		485		490		495
258	Pro Asp Leu Ser	Leu His Leu Pro Asp	Asn Arg Ile Arg Trp Lys			
259		500		505		510
261	Ala Leu Pro Trp	Phe Leu Ser Leu Trp	Gly Leu Leu Leu Met Gly			
262		515		520		525
264	Cys Gly Leu Ser	Leu Ala Ser Thr Arg	Cys Leu Gln Ala Arg Cys			
265		530		535		540
267	Leu His Trp Arg	His Lys Leu Leu Pro	Gln Trp Ile Trp Glu Arg			
268		545		550		555
270	Val Pro Asp Pro	Ala Asn Ser Asn Ser	Gly Gln Pro Tyr Ile Lys			
271		560		565		570
273	Glu Val Ser Leu	Pro Gln Pro Pro Lys	Asp Gly Pro Ile Leu Glu			
274		575		580		585
276	Val Glu Glu Val	Glu Leu Gln Pro Val	Val Glu Ser Pro Lys Ala			
277		590		595		600
279	Ser Ala Pro Ile	Tyr Ser Gly Tyr Glu	Lys His Phe Leu Pro Thr			
280		605		610		615
282	Pro Glu Glu Leu	Gly Leu Leu Val				
283		620				
285	<210> SEQ ID NO: 3					
286	<211> LENGTH: 2646					
287	<212> TYPE: DNA					
288	<213> ORGANISM: Homo sapiens					

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290 <220> FEATURE:
291 <221> NAME/KEY: unsure
292 <222> LOCATON: 2433
293 <223> OTHER INFORMATION: unknown base
295 <400> SEQUENCE: 3
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298 aggagcagcg cgcctcggcg ccggcgaagg tgggcccggc tcggggctcc 100
300 cggaggagcg catgcgggga ggcaggggcg cccctttctg gctgtggccg 150
302 ctgcccaggc tggcgcctgc gctctgttg tgggtgcttt tccagcggac 200
304 ggcgtcccg ggcagcggcg ggcactgca gtgctacgga gttggacct 250
306 tgggcgactt gaactgctcg tgggagcctc ttggggacct gggagccccc 300
308 tccgagttac acctccagag ccaaaagtac cgttccaaac aaacccagac 350
310 ttgtggcagt gcagccggac gtagctgggt ggcattcctc cgggaacagc 400
312 tcaccatgtc tgacaaactc cttgtctygg gactaaggc aggcagacct 450
314 ctctggcccc ccytcttctt gaacctagaa acccaaatga agccaaacgc 500
316 ccccggctcg ggcctcgacg tggacttttc cgaggatgac cccctyggag 550
318 ccactgtcca ttggggccca cctacatggc catctcataa agttctgatc 600
320 tgccagttcc actaccgaag atgtcaggag ggcgctgga cccctgctga 650
322 accggagctg aagaccatac cctgacccc tgttgagatc caagatttgg 700
324 agctagccac tggctacaaa gtgtatggcc gctggcgcat yggaaaagaa 750
326 gaggatttgt ggggcgagtg gagccccatt ttgtccttcc agacaccgcc 800
328 ttctgctcca aaagtgtgtt gggatcagg gaacctctgt gggagcctcg 850
330 gaggagagga acctttgctt ctatggaagg cccagggccc ctgtgtgcag 900
332 gtgagctaca aagtctggtt ctgggttggg ggtcgtgagc tgagtccaga 950
334 aggaattacc tgcctgctct ccttaattcc cagtggggcg gaggggcca 1000
336 ygggtgtcgc tgtcaacgcr acaagctggg agcctctcac caacctctct 1050
338 ttgggtctgt tggattcagc ctctgcccc cgtagcgtgg cagtcaagag 1100
340 catcgtctgg agcagcgagc tactggtgac ctggcaaccg ggcctgagg 1150
342 aaccactgga gcatgtagt gactgggctc gagatgggga cccctgagg 1200
344 aaactcaact gggctcggct tccccctggg aacctcagtg ctctgttacc 1250
346 agggaaattc actgtcgggg tccccctalc aatcactgtg accgcagctc 1300
348 ctgcttcagg cttggcctct gcatcctccg tctggggggt caggggagaa 1350
350 ttgaccccc tagtggggcc aacgctttgg cgaactcaag atgccccctc 1400
352 agggaccccc gccatagcgt ggggagaggt cccaaggcac cagcttcgag 1450
354 gccacctcac ccactacacc ttgtgtgcac agagtggaac cagccccctc 1500
356 gtctgcatga atgtgagtgg caacacacag agtgtcacc tgctgacct 1550
358 tccttggggt cctgtgagc tgtgggtgac agcatctacc atcgtggac 1600
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366 acaaagtgtc gcccgcgtgg gtctgggaga aagttcttga tcctgccaac 1800
368 agcagttcag gccagcccca catggagcaa gtacctgagg cccagccctc 1850
370 tggggacttg cccatcctgg aagtggagga gatggagccc ccgcccgtta 1900
372 tggagtcttc ccagcccgcc caggccaccg ccccgcttga ctctgggtat 1950
374 gagaagcact tctgtccca acctgaggag ctgggcttcc tggggccccc 2000
376 caggccacag gttctggcct gaaccacag tctggctggg ggtgcccagc 2050
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380 tcttgatgga tgaagacact gaggactcag agaggctgag tcacttacct 2150
382 yaggacaccc agccaggcag aytggtgatt yaaggacccc tatagagaag 2200

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/692,504

DATE: 11/02/2000

TIME: 13:57:02

Input Set : A:\P1748R1.txt

Output Set: N:\CRF3\11022000\I692504.raw

L:11 M:282 W: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 3